

WHAT IS CLAIMED IS:

1 1. A method for determining gender from a human DNA sample, said method
2 comprising:
3 providing a human DNA sample, said DNA sample containing X chromosomal material
4 and potentially containing Y chromosomal material;
5 selecting at least one locus from a non-combining X-Y homologous region, said region
6 containing a monomorphic *Alu* insertion in one of the X chromosome and the Y chromosome;
7 amplifying the selected locus of the DNA sample in an amplification reaction, wherein
8 the product of the reaction is a mixture of amplified alleles from the amplified locus present in
9 the sample; and
10 determining the gender of the DNA sample by evaluating the amplified alleles in terms of
11 size and number.

1 2. The method of claim 1, wherein said amplification reaction is a polymerase chain
2 reaction.

1 3. The process of claim 2, wherein the amplification step comprises an amplification of
2 an *AluSTYa* locus.

1 4. The method of claim 3, wherein said amplification step comprises the step of using
2 primer pairs containing the following sequences:

3 Forward 5'- CATGTATTTGATGGGGATAGAGG -3' (SEQ ID NO: 1)

4 and

5 Reverse 5'- CCTTTTCATCCAACTACCACTGA -3' (SEQ ID NO: 2).

1 5. The process of claim 2, wherein the amplification step comprises an amplification of
2 an *AluSTXa* locus.

1 6. The method of claim 5, wherein said amplification step comprises the step of using
2 primer pairs containing the following sequences:

3 Forward 5'- TGAAGAAATTCAGTTCATAGCTTGT -3' (SEQ ID NO: 3)

4 and

5 Reverse 5'- CAGGAGATCCTGAGATTATGTGG -3' (SEQ ID NO: 4).

1 7. The process of claim 2, wherein said amplification step comprises an amplification of
2 an *AluSTXa* locus and an amplification of an *AluSTYa*.

1 8. The method of claim 7, wherein said amplification step comprises the step of using
2 primer pairs containing the following sequences:

3 for said amplification of the *AluSTXa* locus, 5'- TGAAGAAATTCAGTTCATAGCTTGT
4 -3' (SEQ ID NO: 3) and 5'- CAGGAGATCCTGAGATTATGTGG -3' (SEQ ID NO: 4); and
5 for said amplification of the *AluSTYa*, 5'- CATGTATTTGATGGGGATAGAGG -3'
6 (SEQ ID NO: 1) and 5'- CCTTTTCATCCAACTACCACTGA -3' (SEQ ID NO: 2).

1 9. The method of claim 2, wherein at least one primer of each pair has a fluorescent label
2 covalently attached thereto.

1 10. The method of claim 1, wherein the sizes of the amplified alleles are evaluated by
2 fragment resolution on an agarose gel.

1 11. The method of claim 10, wherein the sizes of the amplified alleles are evaluated by
2 comparison with a size standard such that:

3 for a Y insertion *AluSTYa* an *Alu* filled site for Y chromosome has size approximately
4 528 base pairs and an empty site for X chromosome has size approximately 199 base pairs; or

5 for an X insertion *AluSTXa* an *Alu* filled site for X chromosome has size approximately
6 878 base pairs and an empty site for Y chromosome has size approximately 556 base pairs.

1 12. The method of claim 1, wherein male gender is characterized by presence of two
2 DNA fragments and female gender is characterized by presence of one DNA fragment, for
3 amplified loci.

1 13. A primer pair adapted for assaying a Y insertion in a sex determination of human
2 cells, each primer pair having the sequence selected from, or constituting a subset of, the group
3 consisting of:

4 Forward 5'- CATGTATTTGATGGGGATAGAGG -3' (SEQ ID NO: 1)

5 and

6 Reverse 5'- CCTTTTCATCCAACTACCACTGA -3' (SEQ ID NO: 2).

1 14. A primer pair adapted for assaying an X insertion in a sex determination of human
2 cells, each primer having the sequence selected from, or constituting a subset of, the group
3 consisting of:

4 Forward 5'- TGAAGAAATTCAGTTCATAGCTTGT -3' (SEQ ID NO: 3)

5 and

6 Reverse 5'- CAGGAGATCCTGAGATTATGTGG -3' (SEQ ID NO: 4).

1 15. A kit adapted for analyzing alleles of an *AluSTY*a locus on an Y chromosome, said
2 kit comprising a primer pair, each primer of the primer pair having the sequence selected from,
3 or constituting a subset of, the group consisting of:

4 Forward 5'- CATGTATTTGATGGGGATAGAGG -3' (SEQ ID NO: 1)

5 and

6 Reverse 5'- CCTTTTCATCCAACTACCACTGA -3' (SEQ ID NO: 2).

1 16. A kit adapted for analyzing alleles of an *AluSTXa* locus on a X chromosome, said kit
2 comprising a primer pair wherein each primer of the primer pair has the sequence selected from,
3 or constituting a subset of, the group consisting of:

4 Forward 5'- TGAAGAAATTCAGTTCATAGCTTGT -3' (SEQ ID NO: 3)

5 and

6 Reverse 5'- CAGGAGATCCTGAGATTATGTGG -3' (SEQ ID NO: 4).

1 17. A kit for determining gender from a sample, comprising:
2 polymerase chain reaction reagents comprising a polymerase and buffer; and
3 a pair of primers to amplify at least one locus in a non-combining X-Y homologous
4 region of the DNA sample, said locus containing a monomorphic *Alu* insertion.

1 18. The kit of claim 17, wherein said locus is an *AluSTYa* locus.

1 19. The kit of claim 18, wherein said primer pairs containing the following sequences:

2 Forward 5'- CATGTATTTGATGGGGATAGAGG -3' (SEQ ID NO: 1)

3 and

4 Reverse 5'- CCTTTTCATCCAACTACCACTGA -3' (SEQ ID NO: 2).

1 20. The kit of claim 17, wherein said locus is an *AluSTXa* locus.

1 21. The kit of claim 20, wherein said primer pairs containing the following sequences:

2 Forward 5'- TGAAGAAATTCAGTTCATAGCTTGT -3' (SEQ ID NO: 3)

3 and

4 Reverse 5'- CAGGAGATCCTGAGATTATGTGG -3' (SEQ ID NO: 4).

1 22. The kit of claim 17, wherein said at least one locus comprises an *AluSTY*a locus and
2 an *AluSTX*a locus.

1 23. The kit of claim 22, wherein said pair of primers comprises:

2 a first primer pair, wherein each primer of the first primer pair has the sequence selected
3 from, or constituting a subset of, the group consisting of:

4 Forward 5'- TGAAGAAATTCAGTTCATAGCTTGT -3' (SEQ ID NO: 3)

5 and

6 Reverse 5'- CAGGAGATCCTGAGATTATGTGG -3' (SEQ ID NO: 4); and

7 a second primer pair, wherein each primer of the second primer pair has the sequence
8 selected from, or constituting a subset of, the group consisting of:

9 Forward 5'- CATGTATTTGATGGGGATAGAGG -3' (SEQ ID NO: 1)

10 and

11 Reverse 5'- CCTTTTCATCCAACTACCACTGA -3' (SEQ ID NO: 2).

1 24. A method for quantitating male DNA in a sample, said method comprising the steps
2 of:
3 amplifying a locus in the sample by a polymerase chain reaction, wherein said locus is in
4 a non-combining X-Y homologous region and contains a monomorphic *Alu* insertion;
5 detecting the product of the amplified locus; and
6 comparing the detected result with a result of standard male DNA to quantitate DNA in a
7 sample.

1 25. The method of claim 24, wherein the locus is *AluSTYa*, *AluSTXa*, or both *AluSTYa*
2 and *AluSTXa*.

1 26. The method of claim 25, wherein said amplification step comprises the step of using
2 primer pairs containing at least one of the following pair of sequences:

3 5'- TGAAGAAATTCAGTTCATAGCTTGT -3' (SEQ ID NO: 3) and
4 5'- CAGGAGATCCTGAGATTATGTGG -3' (SEQ ID NO: 4); and
5 5'- CATGTATTTGATGGGGATAGAGG -3' (SEQ ID NO: 1) and
6 5'- CCTTTTCATCCAACTACCACTGA -3' (SEQ ID NO: 2).